

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAAAGAACTGACTGA
AACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGTGGCTGTTGGTTTCCAGTCTCTCA
AGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGATGAATTAGCTTCAGGGTTTTTGTGTTCCCTTACCC
ATATCCATTTGCCCCACTTCCACCAATTCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCTATTCCAAT
ACCTGAATCTGCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAAACAAGAAGGATAAGTCACGATAAACCTGGTCA
CCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAATGTAATTGAA
ATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACATGAAAGCAAAGATTTTGGTTTC
TTAATTTCCACA

FIGURE 2

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGCGGAGCCAGACGCTG
ACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGGAGCC**ATG**CGACCCAGG
GCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCG
CCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGT
GCTTACAAGGGCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGA
TCCCAGGTCCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCA
ACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATTTACAA
AGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTC
AGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACC
AAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTG
GTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGAT
GGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TAA**ATGCTTTAATTTTCATTTGCTACCTCTTTTT
TTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAA
AAGTGGTTTCAATATTTTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGA
ATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTTAAAAAATATAAAAGCTACCAATCTTTGTAC
AATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

FIGURE 3

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCGGCAGCCCCGCCG
 CCCCCGAGCCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGA
 AGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCGGGGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTG
 GCTGGGACCCGACCGCTGCCGGCCGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAAACCCAGCCCGGCCGCCG
 CCTGGGCAAGGCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCAGCCTCTTGGGGGAGAGTCCAT
 CTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCCAAGCA
 GTACCCCTGTTCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGGGCCGCGCATAGCTCCGACTACAGCATGTG
 GAGGAAGAACCAGTACGTAGTAACGGGCTGCGCGACTTTGCGGAGCGCGCGAGGCCTGGGCGCTGATGAAGGA
 GATCGAGGCGGCGGGGAGGCGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGG
 GCAGACGTTCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCCAGCCC
 CGACTGGTTCGTGGGCGTGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGGAACAGGCGGCGCTGGACCT
 GTACCCCTACGACGCCGGGACGGACAGCGGCTTACCTTCTCCTCCCCAACTTCGCCACCATCCCGCAGGACAC
 GGTGACCGAGATAACGTCTCCTCTCCCAGCCACCCGGCCAACTCCTTCTACTACCGCGGGCTGAAGGCCCTGCC
 TCCCATCGCCAGGGTGACACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCC
 CAGCAGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCTGTGGTC
 GTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGACTCGCTACGTCCGGGTCCAGCC
 CGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAGGCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCA
 GAGCCCCGAGCCCCCTGGGGCCCCCGGAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGG
 CCGAGGGCACAGGGGGTTTTGCGGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCC
 TCTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGGCCCCCGTGTCCC
 GTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTT
 ATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCGTCCAGGGGCCTGGCTCCACGTGGTTGCAGATACCTCA
 GACCTGGTGCTCTAGGCTGTGCTGAGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAAT
 AAATGGGGCGGTTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCTGT
 TGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 4

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTACCAATCCCGTGCGCCGCGG
 CTGGGCCGTGCGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCAGGGGTCCGCCGCCA
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAATATTTTTGGGGACAGATTGTGATGCTTGATTACCCCT
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
 TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
 AGTGTCCAAAACCTGCAAGCAGTAGAGAAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
 CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATGGAAAGAAGAGAATTTGATGC
 TGCTGTTAATTCTGGAGAAGTGTGGTTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTTAACTGTGTGATGATGAAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAAATA
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAAGTTTG
 GACAGGAAATTTGTCAACTCCATACAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAAAA
 AGGAGGAGATTGTTTGACTTCACAGACAGCTCAGGCTTAGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAA
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTTCGGCAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTTATTTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAACT
 AAAAAGTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTGTCTCTGCACCAGACATCTGTAGTAA
 TCTGTATGTTTTTCAAGCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAAATTCATCATGGAAA
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTCATGTTACCACGCTTGGACCTCAAAA
 TTTTCTGCCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT
 ACCAGATTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATG
 GGGACTCTGTAACATGTATAACATTCAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTCATGAGTA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
 ACCCACCACCTTCAACGAAGTATGTTACACAAGAAAGACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
 GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGAAATGGCCCCGACATTAAGTGGACTGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT
 TCCCCCAAAATCAAATAAAGCTTATCAGTATCAGATTACAATGGTTGGAATAGGGATGCTTATTCCTGAGAAT
 CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAGTGAAAAAGTTCTACAAGG
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAGAGCA
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAAATTGGAACCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAAGTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAAAGAAATCTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
 GAATTATCTACAGCACTGGTGTAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
 GACTTTGCAAGGCTATAATATATGTTTACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT
 TTTAACAACTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCAAGTCCATG
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGT
 TAGTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAAAACACCCAT
 GATGTGGCAGAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTCTCTCA
 AAGTTGAAAAAATGCTTTTAAATTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
 AAATTTGAGCAACAGTAAGTGCACAAATTTCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
 TAGCAATTAAGTGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
 TGTGTTTATGATTTTCTGAAATTTGCTTTTATAGAAATTTTCCACTGATAGTTGATTTTTGAGGCATCTAATAT
 TTACATATTTGCTTCTGAAGTTTGTGTTTACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTGG
 TTTTTCACCTCTGTCCAGTCTATTTATTTTCAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT
 AATGATACGTGAGTTATTTCCAGTTTACTGTTTACTGTGAGGGCTGCCTTTTTCAGATAAATATTTGACATAATA
 ACTGAAGTTATTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTGA
 CTCAAAGAAATCAAAATTTGTGAGTAACATGATGTTGTTTGTATATAATTCAGAGTGTACAGAATGGTAAAAAT
 CCAATCAGTCAAAAGAGGTCAATGAATTTAAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

FIGURE 5

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAACTGTGTCTGTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCCTGTGCGCAGCAGCAAGAGATAC
ATATGCGAGTTCAACCATCCCTAAATAGTCTTTCTCCAATGTGTCTCCTCAAGCAAGATTATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCCTGGGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTCTAGTCTTTT
TCACTTGTACAAACCCAGTTTGTCTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAAGTTTAGCGTATGTTGACTAACAAAAATTCCTTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
CATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCCTACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTTTCGTATATTTAT
TTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAACCTGAATTTAAAG
AATGCTATCTTGAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAAATTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTTAGAAG
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAACCTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTATTGCTCAATAATAAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPPYPYPPFRPLPPIPFPRFPWFRNFPPIPIPES
APTTPLPSEK

Signal sequence.

amino acids 1-17

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FIGURE 7

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGGKQKAQLRQREVVDLYNGMCLQGPAGVPGRDGSPGANVIP
GTPGIPGRDGFKEGKEGECRESFEESWTPNYKQCSWSSLNYGIDLKIAECTFTKMRSNSALRVLFSGSLRLKCR
NACCQRWYFTFNGAECGSLPIEAIITYLDQGSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGD
ASTGWNSVSRIIEELPK

Signal sequence.

amino acids 1-30

N-glycosylation site.

amino acids 186-189

N-myristoylation sites.

amino acids 67-72, 117-122, 163-168, 199-204, 203-208

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FIGURE 8

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLLGA
AHSSDYSMWRKNQYVSNGLRDFEAERGEAWALMKEIEAAGEALQSVHEVFSAPAVPSGTGQTSAELEVQRRHSLVS
FVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSE
YYPRLKALPPIARVTLLRLRQSPRAFIPPAVLPVPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRGLGTS
RTRYVRVQPANNGSPCPELEEEEAECVPDNCV

Signal sequence.

amino acids 1-26

Glycosaminoglycan attachment site.

amino acids 131-134

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 144-147

N-myristoylation sites.

amino acids 26-31, 74-79, 132-137, 134-139, 190-195, 287-292, 290-295

FIGURE 9

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDDQDFYSLLGVSKTASSREIRQAFKKLALKLHPDKNPNNPNAHG
 DFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYRYDFGIYDDDPEIITLERREFDAAVNSGELWF
 VNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNCGDDRLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESL
 VSFAMQHVRSVTTELWTGNFVNSIQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHN
 LPDFELLSANTLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQPSLA
 VFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWCPPCRALLPELRRASNL
 LYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEHEGHSAAEQILEFIEDLMNPSVVSLTPTTFNELVT
 QRKHNEVVMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQ
 YHSYNGWNRDAYSLRIWGLGFLPQVSTDLTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIKGV
 KAGKVDCQAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGRNKDEL

Signal sequence.

amino acids 1-48

N-glycosylation site.

amino acids 484-487

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 445-448

N-myristoylation sites.

amino acids 2-7, 41-46, 103-108, 110-115, 157-162, 182-187, 243-248, 458-463,
 566-571

Amidation sites.

amino acids 389-392, 739-742

Endoplasmic reticulum targeting sequence.

amino acids 744-748

Cytochrome c family heme-binding site signature.

amino acids 158-163

Thioredoxin.

amino acids 128-234, 406-509, 511-592, 623-703

DnaJ domain.

amino acids 35-100

FIGURE 10

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGD LKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDEFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLFSSQSAQGKWSDEACRSSKRYICEFTIPK

Signal peptide.

amino acids 1-31

N-myristoylation sites.

amino acids 14-20, 155-161

Amidation sites.

amino acids 126-130, 170-174

C-type lectin domain signature.

amino acids 176-201